

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/390,207

DATE: 09/21/1999  
TIME: 16:08:59

Input Set: I390207.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1 <110> APPLICANT: Thomason, Arlen  
2 Liu, Benxian  
3 <120> TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides  
4 <130> FILE REFERENCE: 99-371  
5 <140> CURRENT APPLICATION NUMBER: US/09/390,207  
6 <141> CURRENT FILING DATE: 1999-09-07  
7 <160> NUMBER OF SEQ ID NOS: 41  
8 <170> SOFTWARE: PatentIn Ver. 2.0  
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19 acctgaggac ccgagccatt g atg gac tcg gac gag acc ggg ttc gag cac 171  
20 Met Asp Ser Asp Glu Thr Gly Phe Glu His  
21 1 5 10  
22 tca gga ctg tgg gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc 219  
23 Ser Gly Leu Trp Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys  
24 15 20 25  
25 cag gca cac ccc atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc 267  
26 Gln Ala His Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly  
27 30 35 40  
28 caa gtc cgg cag cgg tac ctc tac aca gat gat gcc cag cag aca gaa 315  
29 Gln Val Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu  
30 45 50 55  
31 gcc cac ctg gag atc agg gag gat ggg acg gtg ggg ggc gct gct gac 363  
32 Ala His Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp  
33 60 65 70  
34 cag agc ccc gaa agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt 411  
35 Gln Ser Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val  
36 75 80 85 90  
37 att caa atc ttg gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca 459  
38 Ile Gln Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro  
39 95 100 105  
40 gat ggg gcc ctg tat gga tcg ctc cac ttt gac cct gag gcc tgc agc 507  
41 Asp Gly Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser  
42 110 115 120  
43 ttc cgg gag ctg ctt ctt gag gac gga tac aat gtt tac cag tcc gaa 555  
44 Phe Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu

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47       Ala His Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg  
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49       gac cct gca ccc cga gga cca gct cgc ttc ctg cca cta cca ggc ctg       651  
50       Asp Pro Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu  
51       155                   160                   165                   170  
52       ccc ccc gca ccc ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc       699  
53       Pro Pro Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro  
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56       Asp Val Gly Ser Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly  
57                   190                   195                   200  
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59       Arg Ser Pro Ser Tyr Ala Ser  
60                   205                   210  
61       ctttatttat taggttattt atcttattta tttttttatt tttcttactt gagataataa       861  
62       agagttccag aggaggataa gaatgagcat gtgtgagtgt ctgagggaag acatggcagc       921  
63       tggtttgtct cccttggccc ggacaatccc ctctacacct cccctcacgt ggtccgaggg       981  
64       tcctggtctt ccaactgggcc tcaactttttt cttttctttt cttttctttt ttttgagacg       1041  
65       gagtctcgct ctgcactcca gccaggcca cagagcgaga ttccatctca aaaaaataaa       1101  
66       taaataaata aataaataaa tataaaaaata aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa       1161  
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76                   20                   25                   30  
77       Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr  
78                   35                   40                   45  
79       Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg  
80                   50                   55                   60  
81       Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu  
82                   65                   70                   75                   80  
83       Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val  
84                   85                   90                   95  
85       Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly  
86                   100                   105                   110  
87       Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu  
88                   115                   120                   125  
89       Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu  
90                   130                   135                   140  
91       His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly  
92                   145                   150                   155                   160  
93       Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu  
94                   165                   170                   175

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110           1           5           10           15
111      ctg ctg ctg gct gtc ttc ctg ctg ggg gtc tac caa gca tac ccc atc      96
112      Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile
113           20           25           30
114      cct gac tcc agc ccc ctc ctc cag ttt ggg ggt caa gtc cgg cag agg      144
115      Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg
116           35           40           45
117      tac ctc tac aca gat gac gac caa gac act gaa gcc cac ctg gag atc      192
118      Tyr Leu Tyr Thr Asp Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile
119           50           55           60
120      agg gag gat gga aca gtg gta ggc gca gca cac cgc agt cca gaa agt      240
121      Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser
122           65           70           75           80
123      ctc ctg gag ctc aaa gcc ttg aag cca ggg gtc att caa atc ctg ggt      288
124      Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly
125           85           90           95
126      gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat gga gct ctc tat      336
127      Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr
128           100          105          110
129      gga tcg cct cac ttt gat cct gag gcc tgc agc ttc aga gaa ctg ctg      384
130      Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu
131           115          120          125
132      ctg gag gac ggt tac aat gtg tac cag tct gaa gcc cat ggc ctg ccc      432
133      Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro
134           130          135          140
135      ctg cgt ctg cct cag aag gac tcc cca aac cag gat gca aca tcc tgg      480
136      Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp
137           145          150          155          160
138      gga cct gtg cgc ttc ctg ccc atg cca ggc ctg ctc cac gag ccc caa      528
139      Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln
140           165          170          175
141      gac caa gca gga ttc ctg ccc cca gag ccc cca gat gtg ggc tcc tct      576
142      Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser
143           180          185          190
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158              20                      25                      30
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160              35                      40                      45
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162              50                      55                      60
163      Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser
164              65                      70                      75                      80
165      Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly
166              85                      90                      95
167      Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr
168              100                     105                     110
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170              115                     120                     125
171      Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro
172              130                     135                     140
173      Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp
174              145                     150                     155                     160
175      Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln
176              165                     170                     175
177      Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser
178              180                     185                     190
179      Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser Pro Ser Tyr
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181      Ala Ser
182              210
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186      <213> ORGANISM: Homo sapiens
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191              20                      25                      30
192      Leu Glu Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser
193              35                      40                      45
194      Pro Glu Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln

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196 Ile Leu Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly
197           65           70           75           80
198 Ala Leu Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg
199           85           90           95
200 Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
201           100          105          110
202 Gly Leu Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro
203           115          120          125
204 Ala Pro Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro
205           130          135          140
206 Ala Pro Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val
207           145          150          155          160
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215 <213> ORGANISM: Mus musculus
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220           20           25           30
221 Leu Glu Ile Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser
222           35           40           45
223 Pro Glu Ser Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln
224           50           55           60
225 Ile Leu Gly Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly
226           65           70           75           80
227 Ala Leu Tyr Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg
228           85           90           95
229 Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His
230           100          105          110
231 Gly Leu Pro Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala
232           115          120          125
233 Thr Ser Trp Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His
234           130          135          140
235 Glu Pro Gln Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val
236           145          150          155          160
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242 <211> LENGTH: 21
243 <212> TYPE: DNA
244 <213> ORGANISM: Mus musculus

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**Please Note:**  
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the  
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
<223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY  
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DATE: 09/21/1999  
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Line	Error/Warning	Original Text
60	W Invalid/Missing Amino Acid Numbering	205 210
935	W "N" or "Xaa" used: Feature required	ggaaggaaaa aagcggccgc aacannnnnn nnn